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 Katsuya, OZAKI  
 Katsutoshi, ARA  
 Shuji, KAWAI  
 Susumu, ITO  
 <120> TITLE OF INVENTION: GENE ENCODING ALKALINE LIQUEFYING ALPHA-AMYLASE  
 <130> FILE REFERENCE: 2173-106P  
 <140> CURRENT APPLICATION NUMBER:10829331  
 <141> CURRENT FILING DATE:2004-04-22  
 <150> PRIOR APPLICATION NUMBER: US/08/952,741  
 <151> PRIOR FILING DATE: 1997-11-25  
 <160> NUMBER OF SEQ ID NOS: 11  
 <170> SOFTWARE: PatentIn Ver. 2.0  
 <210> SEQ ID NO 1  
 <211> LENGTH: 1776  
 <212> TYPE: DNA  
 <213> ORGANISM: Bacillus sp.  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (145)..(1692)  
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 120  
 aaattgaagg agaggggtgct tttt atg aaa ctt cat aac cgt ata att agc  
 171  
 Met Lys Leu His Asn Arg Ile Ile Ser  
 1 5  
 gta cta tta aca cta ttg tta gct gta gct gtt ttg ttt cca tat atg  
 219  
 Val Leu Leu Thr Leu Leu Leu Ala Val Ala Val Leu Phe Pro Tyr Met  
 10 15 20 25  
 acg gaa cca gca caa gcc cat cat aat ggg acg aat ggg acc atg atg  
 267  
 Thr Glu Pro Ala Gln Ala His His Asn Gly Thr Asn Gly Thr Met Met  
 30 35 40  
 cag tat ttt gaa tgg cat ttg cca aat gac ggg aac cac tgg aac agg  
 315  
 Gln Tyr Phe Glu Trp His Leu Pro Asn Asp Gly Asn His Trp Asn Arg  
 45 50 55  
 tta cga gat gac gca gct aac tta aag agt aaa ggg att acc gct gtt  
 363  
 Leu Arg Asp Asp Ala Ala Asn Leu Lys Ser Lys Gly Ile Thr Ala Val  
 60 65 70  
 tgg att cct cct gca tgg aag ggg act tcg caa aat gat gtt ggg tat  
 411  
 Trp Ile Pro Pro Ala Trp Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr  
 75 80 85  
 ggt gcc tat gat ttg tac gat ctt ggt gag ttt aac caa aag gga acc  
 459  
 Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr  
 90 95 100 105  
 gtc cgt aca aaa tat ggc aca agg agt cag ttg caa ggt gcc gtg aca  
 507  
 Val Arg Thr Lys Tyr Gly Thr Arg Ser Gln Leu Gln Gly Ala Val Thr  
 110 115 120

555 tct ttg aaa aat aac ggg att caa gtt tat ggg gat gtc gtg atg aat  
 Ser Leu Lys Asn Asn Gly Ile Gln Val Tyr Gly Asp Val Val Met Asn  
 125 130 135  
 603 cat aaa ggt gga gca gac ggg aca gag atg gta aat gcg gtg gaa gtg  
 His Lys Gly Gly Ala Asp Gly Thr Glu Met Val Asn Ala Val Glu Val  
 140 145 150  
 651 aac cga agc aac cga aac caa gaa ata tca ggt gaa tac acc att gaa  
 Asn Arg Ser Asn Arg Asn Gln Glu Ile Ser Gly Glu Tyr Thr Ile Glu  
 155 160 165  
 699 gca tgg acg aaa ttt gat ttc cct gga aga gga aat acc cat tcc aac  
 Ala Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly Asn Thr His Ser Asn  
 170 175 180 185  
 747 ttt aaa tgg cgc tgg tat cat ttt gat ggg aca gat tgg gat cag tca  
 Phe Lys Trp Arg Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Gln Ser  
 190 195 200  
 795 cgt cag ctt cag aac aaa ata tat aaa ttc aga ggt acc gga aag gca  
 Arg Gln Leu Gln Asn Lys Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala  
 205 210 215  
 843 tgg gac tgg gaa gta gat ata gag aac ggc aac tat gat tac ctt atg  
 Trp Asp Trp Glu Val Asp Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met  
 220 225 230  
 891 tat gca gac att gat atg gat cat cca gaa gta atc aat gaa ctt aga  
 Tyr Ala Asp Ile Asp Met Asp His Pro Glu Val Ile Asn Glu Leu Arg  
 235 240 245  
 939 aat tgg gga gtt tgg tat aca aat aca ctt aat cta gat gga ttt aga  
 Asn Trp Gly Val Trp Tyr Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg  
 250 255 260 265  
 987 atc gat gct gtg aaa cat att aaa tac agc tat acg aga gat tgg cta  
 Ile Asp Ala Val Lys His Ile Lys Tyr Ser Tyr Thr Arg Asp Trp Leu  
 270 275 280  
 1035 aca cat gtg cgt aac acc aca ggt aaa cca atg ttt gca gtt gca gaa  
 Thr His Val Arg Asn Thr Thr Gly Lys Pro Met Phe Ala Val Ala Glu  
 285 290 295  
 1083 ttt tgg aaa aat gac ctt gct gca atc gaa aac tat tta aat aaa aca  
 Phe Trp Lys Asn Asp Leu Ala Ala Ile Glu Asn Tyr Leu Asn Lys Thr  
 300 305 310  
 1131 agt tgg aat cac tcc gtg ttc gat gtt cct ctt cat tat aat ttg tac  
 Ser Trp Asn His Ser Val Phe Asp Val Pro Leu His Tyr Asn Leu Tyr  
 315 320 325  
 1179 aat gca tct aat agt ggt ggc tat ttt gat atg aga aat att tta aat  
 Asn Ala Ser Asn Ser Gly Gly Tyr Phe Asp Met Arg Asn Ile Leu Asn  
 330 335 340 345  
 1227 ggt tct gtc gta caa aaa cac cct ata cat gca gtc aca ttt gtt gat  
 Gly Ser Val Val Gln Lys His Pro Ile His Ala Val Thr Phe Val Asp  
 350 355 360  
 aac cat gac tct cag cca gga gaa gca ttg gaa tcc ttt gtt caa tcg

1275 Asn His Asp Ser Gln Pro Gly Glu Ala Leu Glu Ser Phe Val Gln Ser  
365 370 375  
tgg ttc aaa cca ctg gca tat gca ttg att ctg aca agg gag caa ggt

1323 Trp Phe Lys Pro Leu Ala Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly  
380 385 390  
tac cct tcc gta ttt tac ggt gat tac tac ggt ata cca act cat ggt

1371 Tyr Pro Ser Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly  
395 400 405  
gtt cct tcg atg aaa tct aaa att gat cca ctt ctg cag gca cgt caa

1419 Val Pro Ser Met Lys Ser Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln  
410 415 420 425  
acg tat gcc tac gga acc caa cat gat tat ttt gat cat cat gat att

1467 Thr Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His His Asp Ile  
430 435 440  
atc ggc tgg acg aga gaa ggg gac agc tcc cac cca aat tca gga ctt

1515 Ile Gly Trp Thr Arg Glu Gly Asp Ser Ser His Pro Asn Ser Gly Leu  
445 450 455  
gca act att atg tcc gat ggg cca ggg ggt aat aaa tgg atg tat gtc

1563 Ala Thr Ile Met Ser Asp Gly Pro Gly Gly Asn Lys Trp Met Tyr Val  
460 465 470  
ggg aaa cat aaa gct ggc caa gta tgg aga gat atc acc gga aat agg

1611 Gly Lys His Lys Ala Gly Gln Val Trp Arg Asp Ile Thr Gly Asn Arg  
475 480 485  
tct ggt acc gtc acc att aat gca gat ggt tgg ggg aat ttc act gta

1659 Ser Gly Thr Val Thr Ile Asn Ala Asp Gly Trp Gly Asn Phe Thr Val  
490 495 500 505  
aac gga ggg gca gtt tcg gtt tgg gtg aag caa taaataagga acaagaggcg

1712 Asn Gly Gly Ala Val Ser Val Trp Val Lys Gln  
510 515  
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1772 gctt

1776

<210> SEQ ID NO 2

<211> LENGTH: 516

<212> TYPE: PRT

<213> ORGANISM: Bacillus sp.

<400> SEQUENCE: 2

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Ala Val Ala Val Leu Phe Pro Tyr Met Thr Glu Pro Ala Gln Ala His  
20 25 30  
His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His Leu  
35 40 45  
Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala Asn  
50 55 60  
Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp Lys  
65 70 75 80  
Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp  
85 90 95

Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	
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Arg	Ser	Gln	Leu	Gln	Gly	Ala	Val	Thr	Ser	Leu	Lys	Asn	Asn	Gly	Ile	
		115					120					125				
Gln	Val	Tyr	Gly	Asp	Val	Val	Met	Asn	His	Lys	Gly	Gly	Ala	Asp	Gly	
	130					135					140					
Thr	Glu	Met	Val	Asn	Ala	Val	Glu	Val	Asn	Arg	Ser	Asn	Arg	Asn	Gln	
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Glu	Ile	Ser	Gly	Glu	Tyr	Thr	Ile	Glu	Ala	Trp	Thr	Lys	Phe	Asp	Phe	
			165					170						175		
Pro	Gly	Arg	Gly	Asn	Thr	His	Ser	Asn	Phe	Lys	Trp	Arg	Trp	Tyr	His	
			180					185					190			
Phe	Asp	Gly	Thr	Asp	Trp	Asp	Gln	Ser	Arg	Gln	Leu	Gln	Asn	Lys	Ile	
	195						200					205				
Tyr	Lys	Phe	Arg	Gly	Thr	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Asp	Ile	
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Glu	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Met	Asp	
225				230						235					240	
His	Pro	Glu	Val	Ile	Asn	Glu	Leu	Arg	Asn	Trp	Gly	Val	Trp	Tyr	Thr	
			245						250					255		
Asn	Thr	Leu	Asn	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Val	Lys	His	Ile	
		260						265					270			
Lys	Tyr	Ser	Tyr	Thr	Arg	Asp	Trp	Leu	Thr	His	Val	Arg	Asn	Thr	Thr	
	275						280					285				
Gly	Lys	Pro	Met	Phe	Ala	Val	Ala	Glu	Phe	Trp	Lys	Asn	Asp	Leu	Ala	
	290					295					300					
Ala	Ile	Glu	Asn	Tyr	Leu	Asn	Lys	Thr	Ser	Trp	Asn	His	Ser	Val	Phe	
305					310					315					320	
Asp	Val	Pro	Leu	His	Tyr	Asn	Leu	Tyr	Asn	Ala	Ser	Asn	Ser	Gly	Gly	
			325						330					335		
Tyr	Phe	Asp	Met	Arg	Asn	Ile	Leu	Asn	Gly	Ser	Val	Val	Gln	Lys	His	
		340						345					350			
Pro	Ile	His	Ala	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Ser	Gln	Pro	Gly	
		355					360					365				
Glu	Ala	Leu	Glu	Ser	Phe	Val	Gln	Ser	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	
	370					375					380					
Ala	Leu	Ile	Leu	Thr	Arg	Glu	Gln	Gly	Tyr	Pro	Ser	Val	Phe	Tyr	Gly	
385					390					395					400	
Asp	Tyr	Tyr	Gly	Ile	Pro	Thr	His	Gly	Val	Pro	Ser	Met	Lys	Ser	Lys	
			405						410				415			
Ile	Asp	Pro	Leu	Gln	Ala	Arg	Gln	Thr	Tyr	Ala	Tyr	Gly	Thr	Gln		
		420					425					430				
His	Asp	Tyr	Phe	Asp	His	His	Asp	Ile	Ile	Gly	Trp	Thr	Arg	Glu	Gly	
	435						440					445				
Asp	Ser	Ser	His	Pro	Asn	Ser	Gly	Leu	Ala	Thr	Ile	Met	Ser	Asp	Gly	
	450					455					460					
Pro	Gly	Gly	Asn	Lys	Trp	Met	Tyr	Val	Gly	Lys	His	Lys	Ala	Gly	Gln	
465					470					475					480	
Val	Trp	Arg	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Gly	Thr	Val	Thr	Ile	Asn	
			485						490					495		
Ala	Asp	Gly	Trp	Gly	Asn	Phe	Thr	Val	Asn	Gly	Gly	Ala	Val	Ser	Val	
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Trp	Val	Lys	Gln													
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<210> SEQ ID NO 3  
 <211> LENGTH: 22  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: any n = a,c,t or g

<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer  
<400> SEQUENCE: 3  
tngaygcngt naarcayath aa

22

<210> SEQ ID NO 4  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: any n = a,c,t or g  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer  
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26

<210> SEQ ID NO 5  
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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer  
<400> SEQUENCE: 5  
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23

<210> SEQ ID NO 6  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer  
<400> SEQUENCE: 6  
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<210> SEQ ID NO 7  
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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer  
<400> SEQUENCE: 7  
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20

<210> SEQ ID NO 8  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer  
<400> SEQUENCE: 8  
catttggaac atgccattca aa

22

<210> SEQ ID NO 9  
<211> LENGTH: 21  
<212> TYPE: DNA